Figure 1A
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```
  1  ATGAGCTCCCGCATCGCCAGGGCGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG   60
  1  M  S  S  R  I  A  R  A  L  A  L  V  V  T  L  L  H  L  T  R    20

 61  CTGGCGCTCTCCACCTGCCCCGCTGCCTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG  120
 21  L  A  L  S  T  C  P  A  A  C  H  C  P  L  E  A  P  K  C  A    40

121  CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGCTGTAAGGTCTGCGCCAAGCAGCTC  180
 41  P  G  V  G  L  V  R  D  G  C  G  C  C  K  V  C  A  K  Q  L    60

181  AACGAGGACTGCAGCAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC  240
 61  N  E  D  C  S  K  T  Q  P  C  D  H  T  K  G  L  E  C  N  F    80

241  GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT  300
 81  G  A  S  S  T  A  L  K  G  I  C  R  A  Q  S  E  G  R  P  C   100

301  GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG  360
101  E  Y  N  S  R  I  Y  Q  N  G  E  S  F  Q  P  N  C  K  H  Q   120

361  TGCACATGTATTGATGGCGCCGTGGGCTGCATTCCTCTGTGTCCCCAAGAACTATCTCTC  420
121  C  T  C  I  D  G  A  V  G  C  I  P  L  C  P  Q  E  L  S  L   140

421  CCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAGGAG  480
141  P  N  L  G  C  P  N  P  R  L  V  K  V  T  G  Q  C  C  E  E   160

481  TGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTTGGC  540
161  W  V  C  D  E  D  S  I  K  D  P  M  E  D  Q  D  G  L  L  G   180

541  AAGGAGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATTGCA  600
181  K  E  L  G  F  D  A  S  E  V  E  L  T  R  N  N  E  L  I  A   200

601  GTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATCCTA  660
201  V  G  K  G  S  S  L  K  R  L  P  V  F  G  M  E  P  R  I  L   220

661  TACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGCTCA  720
221  Y  N  P  L  Q  G  Q  K  C  I  V  Q  T  T  S  W  S  Q  C  S   240

721  AAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGCCTT  780
241  K  T  C  G  T  G  I  S  T  R  V  T  N  D  N  P  E  C  R  L   260

781  GTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGCCTG  840
261  V  K  E  T  R  I  C  E  V  R  P  C  G  Q  P  V  Y  S  S  L   280
```

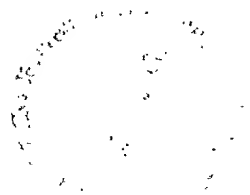

Figure 1B
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```
841  AAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACTTAC  900
281  K  K  G  K  K  C  S  K  T  K  K  S  P  E  P  V  R  F  T  Y   300

901  GCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGACGGC  960
301  A  G  C  L  S  V  K  K  Y  R  P  K  Y  C  G  S  C  V  D  G   320

961  CGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCGCTGCGAAGATGGG  1020
321  R  C  C  T  P  Q  L  T  R  T  V  K  M  R  F  R  C  E  D  G   340

1021 GAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTGCAAATGCAACTACAACTGCCCG  1080
341  E  T  F  S  K  N  V  M  M  I  Q  S  C  K  C  N  Y  N  C  P   360

1081 CATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCAATGACATTCACAAATTTAGG  1140
361  H  A  N  E  A  A  F  P  F  Y  R  L  F  N  D  I  H  K  F  R   380

1141 GACTAA  1146
381  D  *    382
```

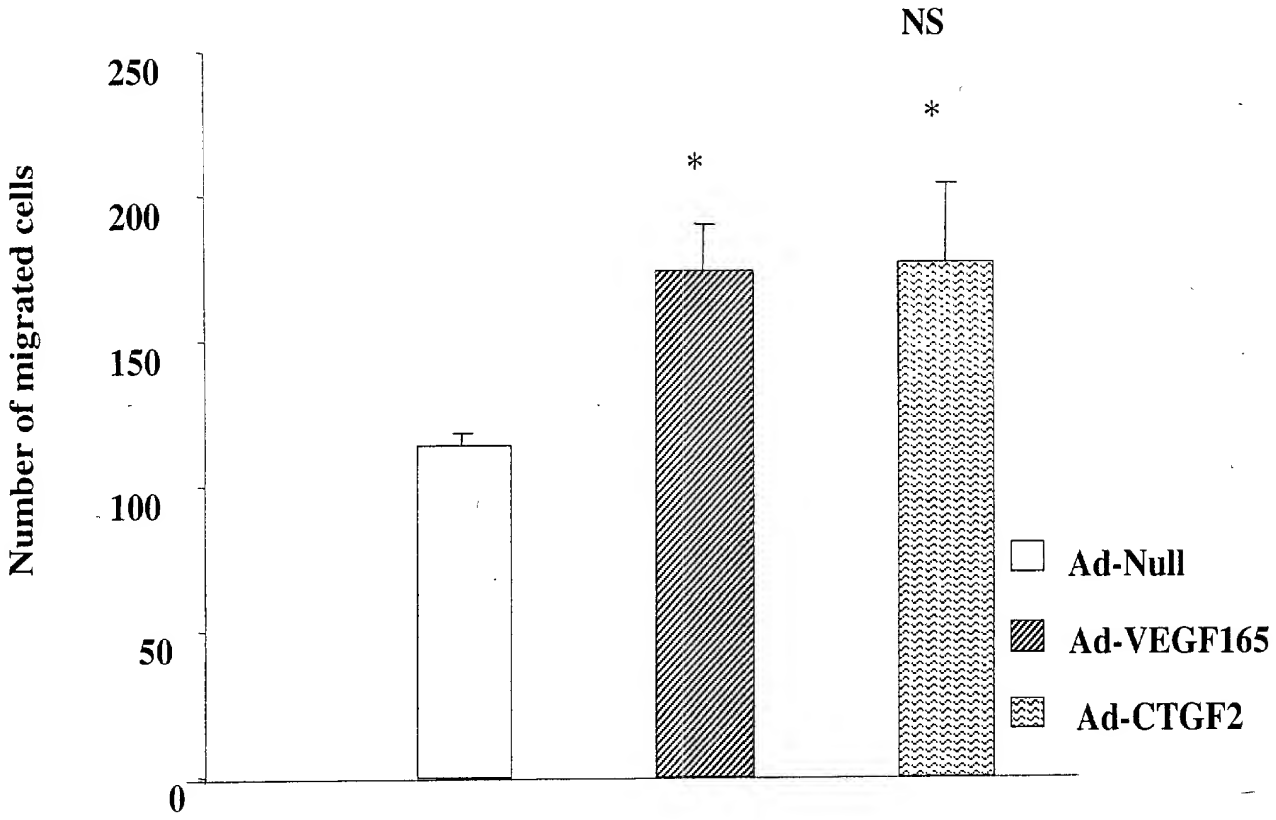

NS
*
*
250
200
150
100
50
0
Number of migrated cells
Ad-Null
Ad-VEGF165
Ad-CTGF2

Figure 2

Figure 3

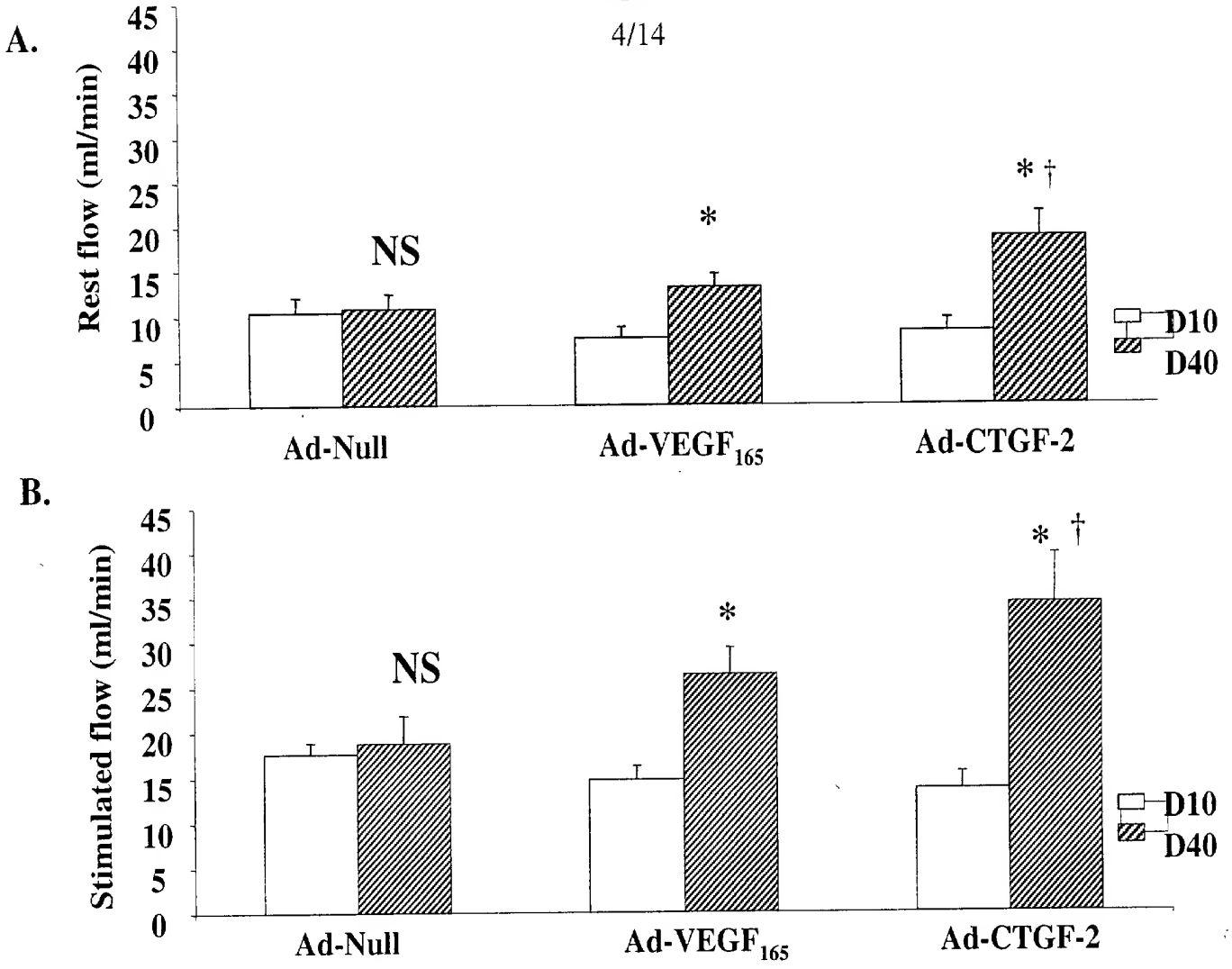

A.
Rest flow (ml/min)
45
40
35
30
25
20
15
10
5
0
NS
*
* †
D10
D40
Ad-Null
Ad-VEGF165
Ad-CTGF-2
B.
Stimulated flow (ml/min)
45
40
35
30
25
20
15
10
5
0
NS
*
* †
D10
D40
Ad-Null
Ad-VEGF165
Ad-CTGF-2

Figure 4

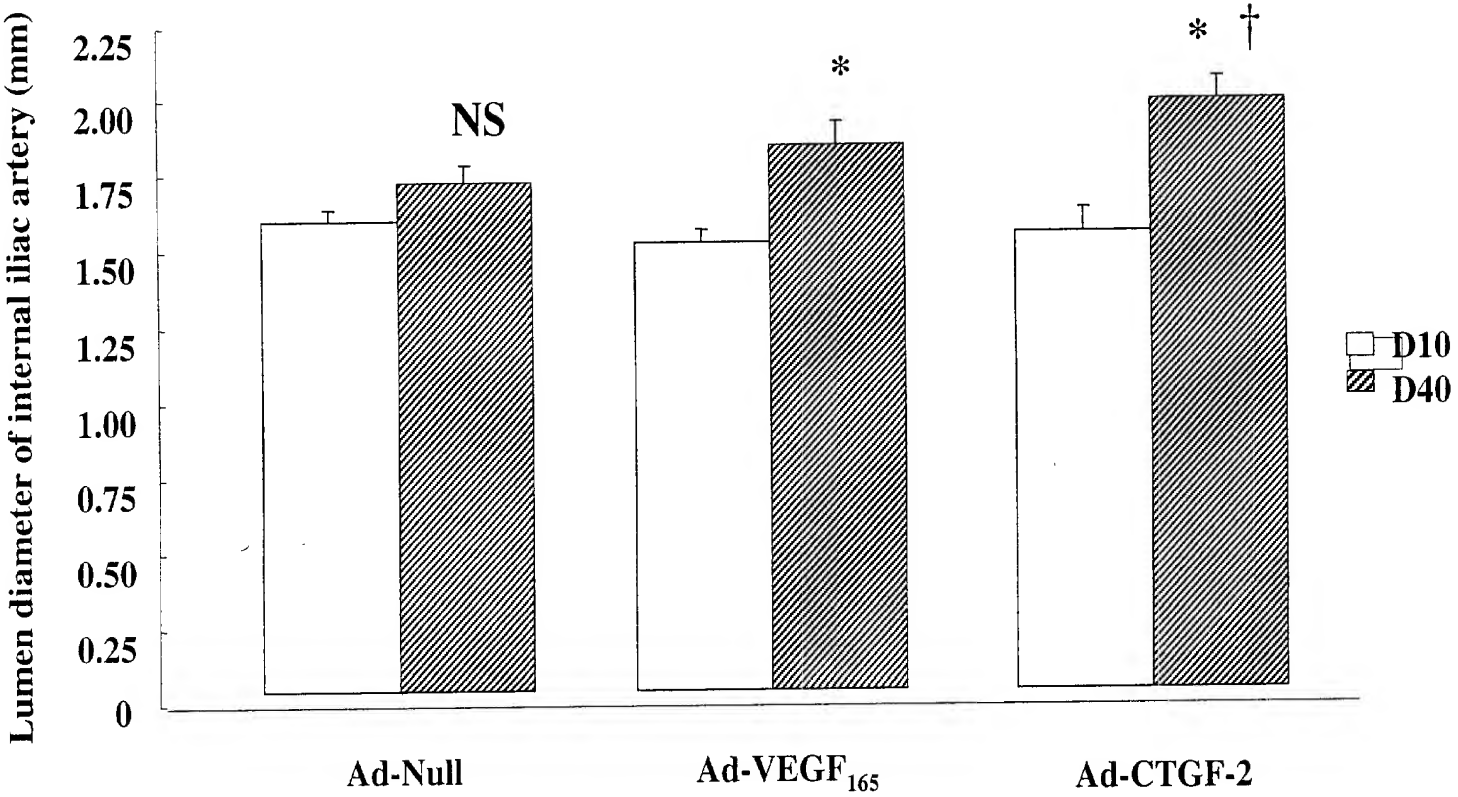
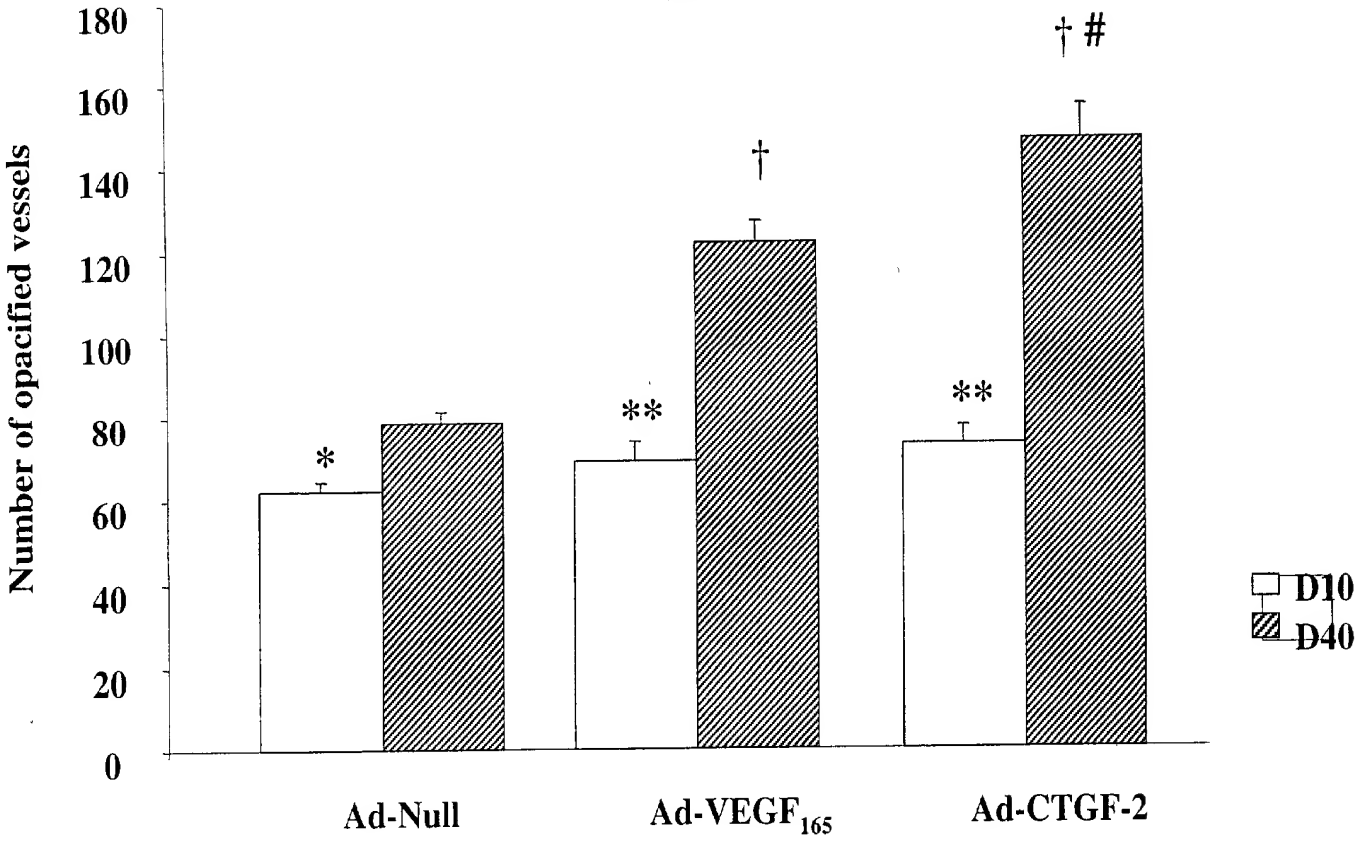

Lumen diameter of internal iliac artery (mm)
2.25
2.00
1.75
1.50
1.25
1.00
0.75
0.50
0.25
0
NS
*
* †
D10
D40
Ad-Null
Ad-VEGF165
Ad-CTGF-2

Figure 5


Number of opacified vessels
180
160
140
120
100
80
60
40
20
0
*
**
†
**
† #
Ad-Null
Ad-VEGF165
Ad-CTGF-2
D10
D40

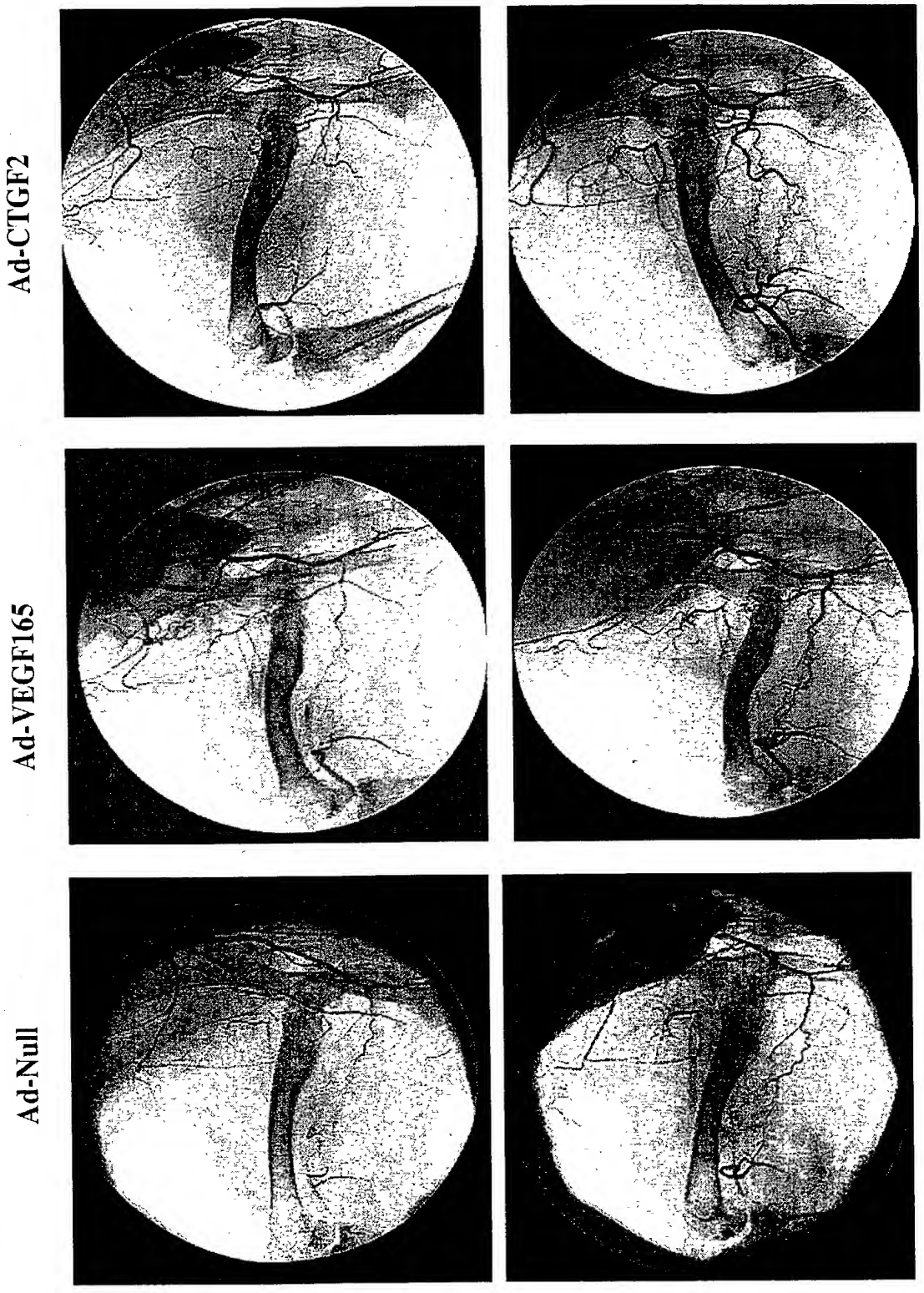


Figure 6

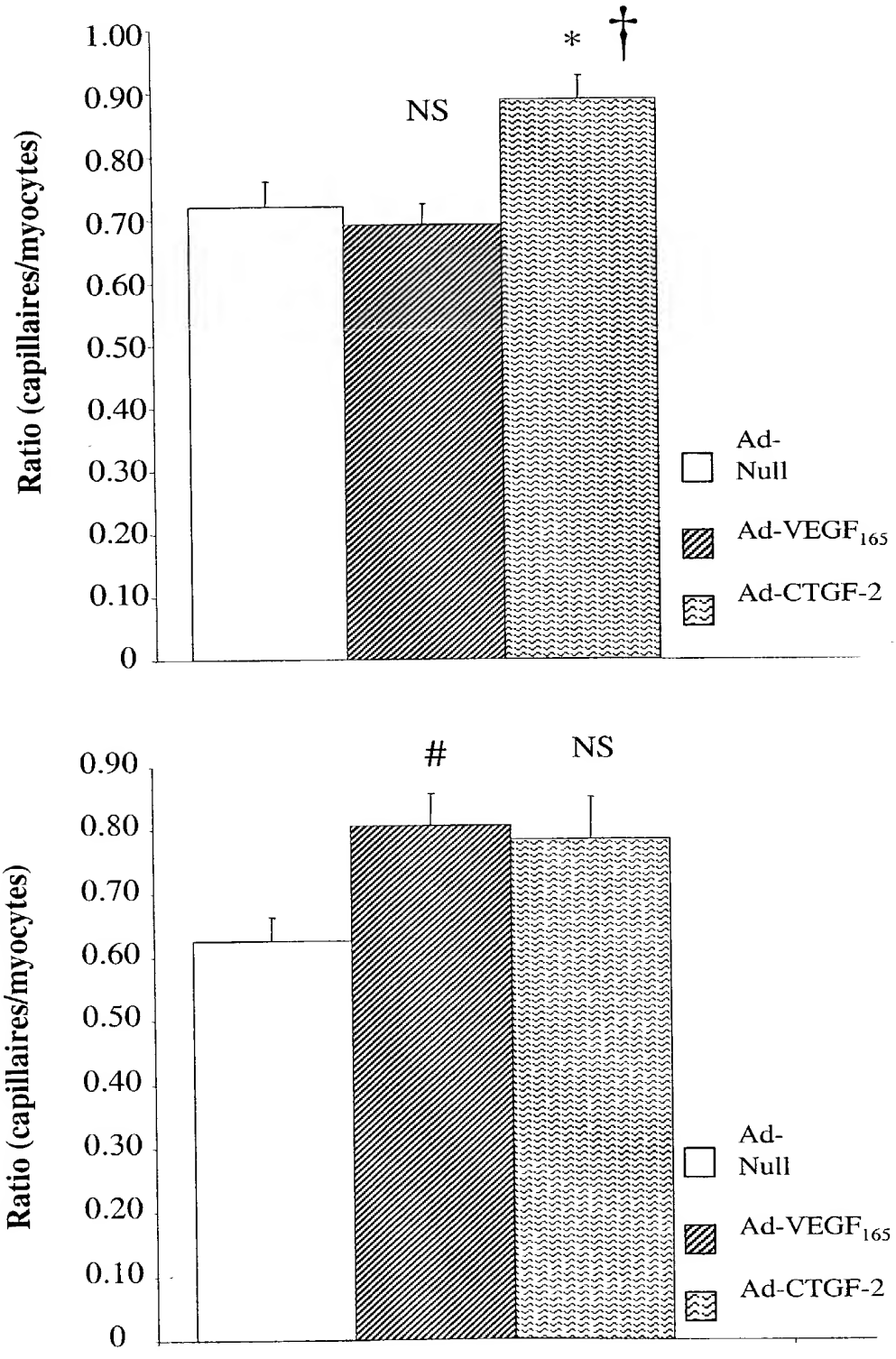

1.00
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0
Ratio (capillaires/myocytes)
NS
*
†
Ad-Null
Ad-VEGF165
Ad-CTGF-2
0.90
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0
Ratio (capillaires/myocytes)
#
NS
Ad-Null
Ad-VEGF165
Ad-CTGF-2

Figure 7

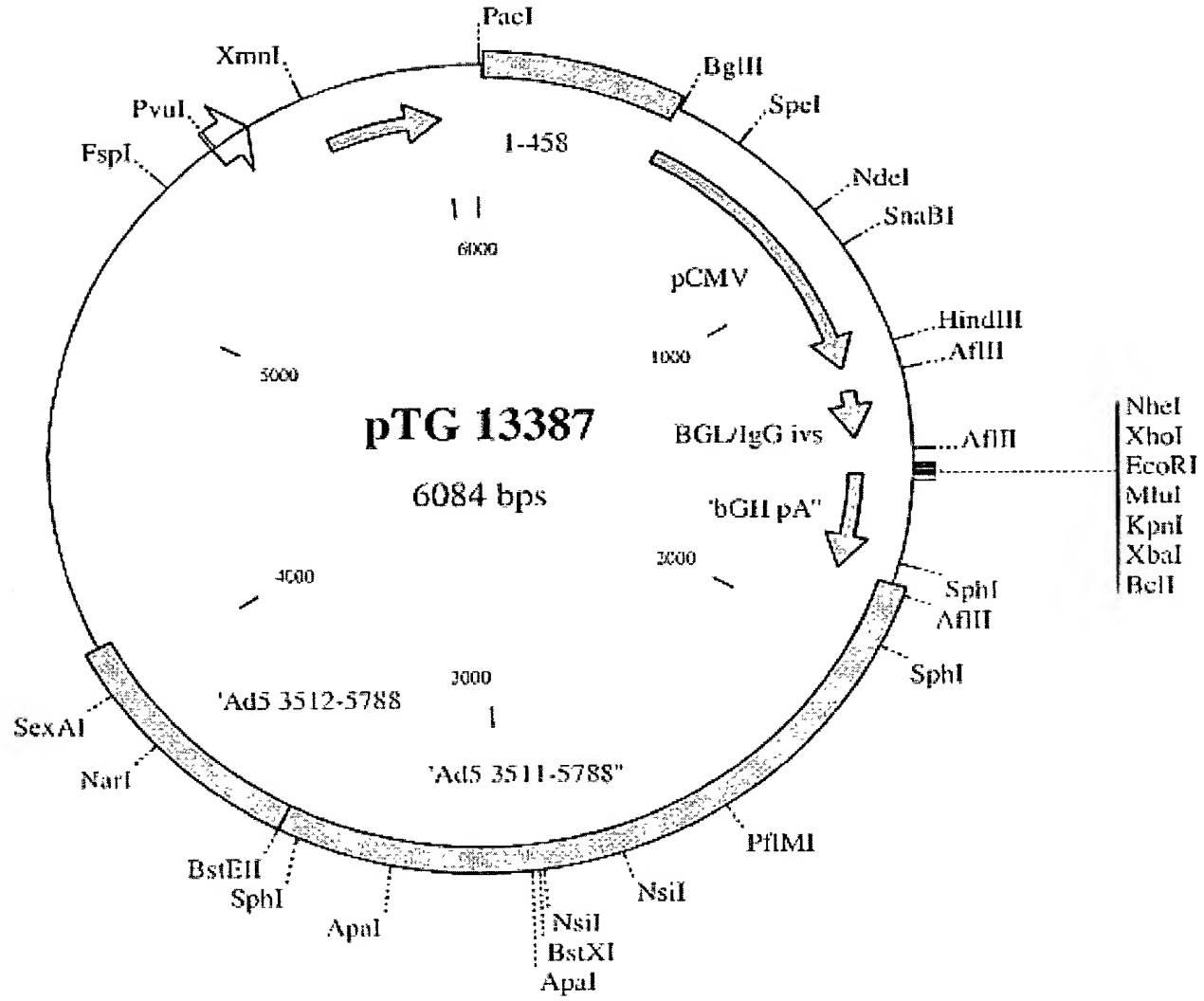

PacI
BglII
SpeI
NdeI
SnaBI
HindIII
AflII
NheI
XhoI
EcoRI
MluI
KpnI
XbaI
BclI
SphI
AflII
SphI
PflMI
NsiI
NsiI
BstXI
ApaI
ApaI
BstEII
SphI
NarI
SexAI
'Ad5 3512-5788
'Ad5 3511-5788"
pTG 13387
6084 bps
1-458
pCMV
BGL/IgG ivs
'bGH pA"
1000
2000
3000
4000
5000
6000
XmnI
PvuI
FspI

Figure 8

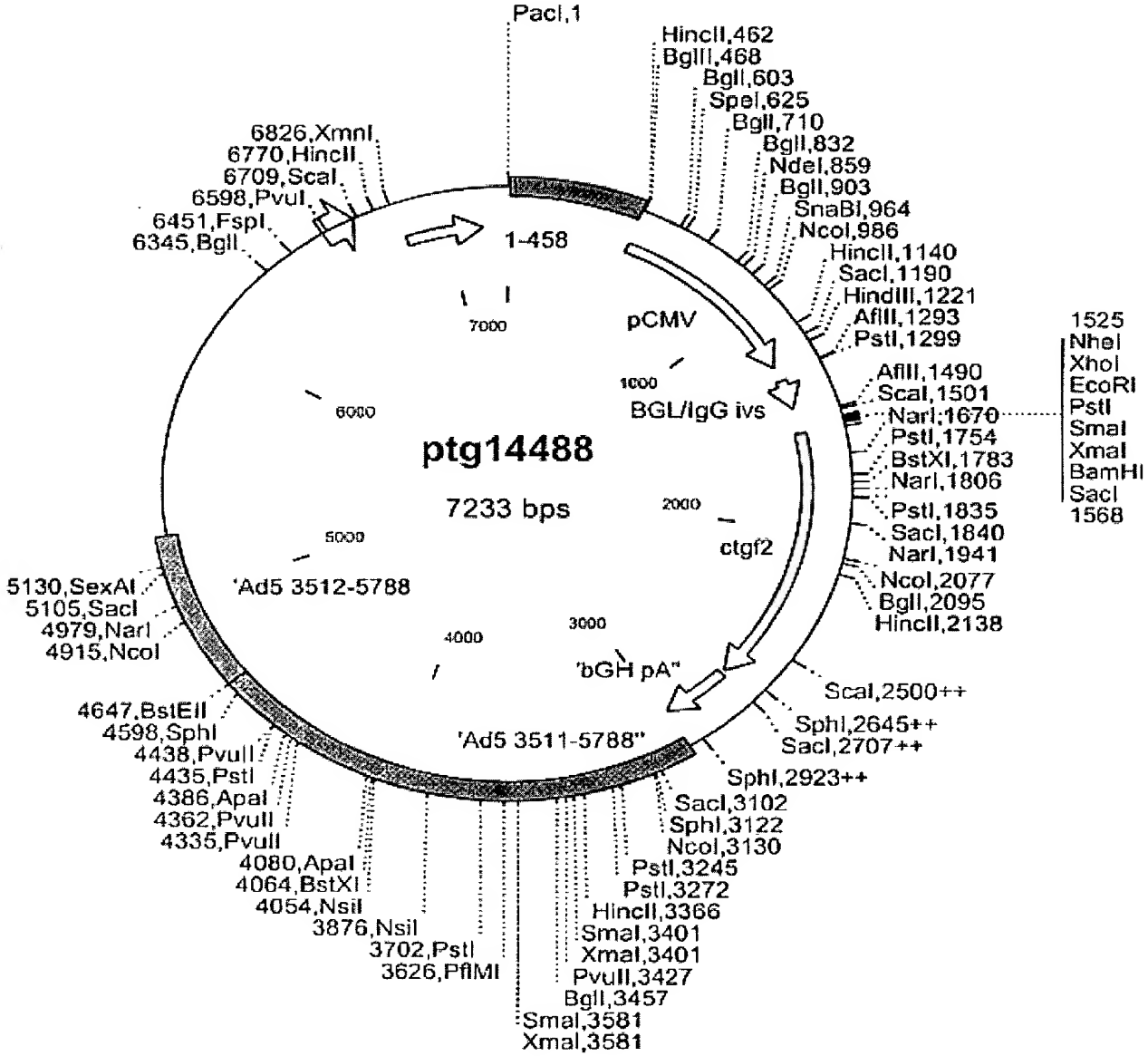

PacI,1
HincII,462
BglII,468
BglI,603
SpeI,625
BglI,710
BglI,832
NdeI,859
BglI,903
SnaBI,964
NcoI,986
HincII,1140
SacI,1190
HindIII,1221
AflII,1293
PstI,1299
AflII,1490
ScaI,1501
NarI,1670
PstI,1754
BstXI,1783
NarI,1806
PstI,1835
SacI,1840
NarI,1941
NcoI,2077
BglI,2095
HincII,2138
ScaI,2500++
SphI,2645++
SacI,2707++
SphI,2923++
SacI,3102
SphI,3122
NcoI,3130
PstI,3245
PstI,3272
HincII,3366
SmaI,3401
XmaI,3401
PvuII,3427
BglI,3457
SmaI,3581
XmaI,3581
4647,BstEII
4598,SphI
4438,PvuII
4435,PstI
4386,ApaI
4362,PvuII
4335,PvuII
4080,ApaI
4064,BstXI
4054,NsiI
3876,NsiI
3702,PstI
3626,PflMI
5130,SexAI
5105,SacI
4979,NarI
4915,NcoI
6826,XmnI
6770,HincII
6709,ScaI
6598,PvuI
6451,FspI
6345,BglI
1525
NheI
XhoI
EcoRI
PstI
SmaI
XmaI
BamHI
SacI
1568
1-458
pCMV
BGL/IgG ivs
ctgf2
'bGH pA"
'Ad5 3511-5788"
'Ad5 3512-5788
ptg14488
7233 bps
1000
2000
3000
4000
5000
6000
7000

Figure 9

Figure 10
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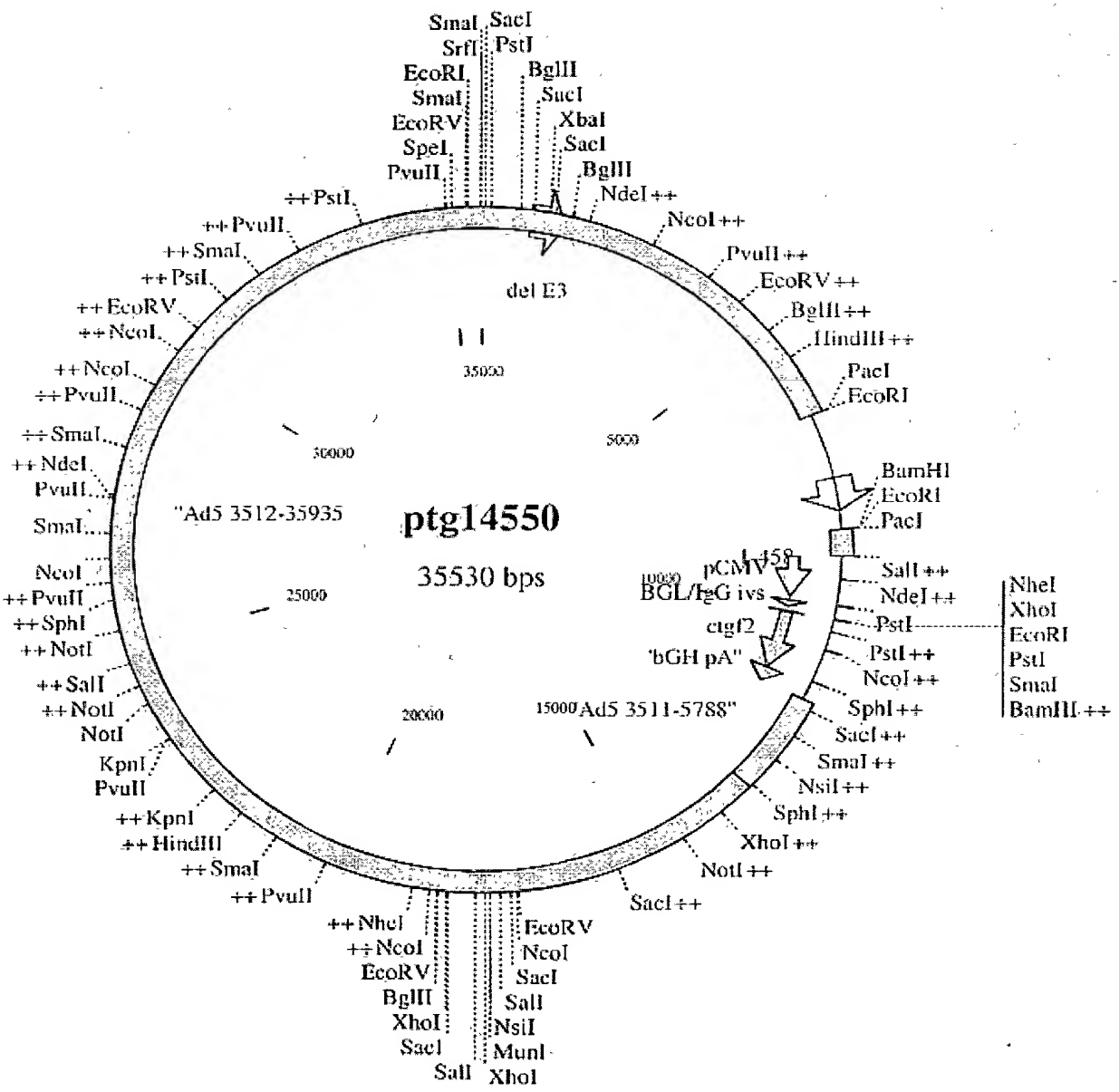

Figure 11A


```
ATGAGCTCCCGAATCGTCAGGGAGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG
M  S  S  R  I  V  R  E  L  A  L  V  V  T  L  L  H  L  T  R

GTGGGGCTCTCCACCTGCCCCGCTGACTGCCACTGCCCCCTGGAGGCGCCCAAGTGCGCG
V  G  L  S  T  C  P  A  D  C  H  C  P  L  E  A  P  K  C  A

CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGTTGTAAGGTCTGCGCCAAGCAGCTC
P  G  V  G  L  V  R  D  G  C  G  C  C  K  V  C  A  K  Q  L

AACGAGGACTGCAGAAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC
N  E  D  C  R  K  T  Q  P  C  D  H  T  K  G  L  E  C  N  F

GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT
G  A  S  S  T  A  L  K  G  I  C  R  A  Q  S  E  G  R  P  C

GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG
E  Y  N  S  R  I  Y  Q  N  G  E  S  F  Q  P  N  C  K  H  Q

TGCACATGTATTGGATGGCGCCGGGGGGCTTGCATTCCTCTGTGTCCCCAAGAACTATCT
C  T  C  I  G  W  R  R  G  A  C  I  P  L  C  P  Q  E  L  S
```

Figure 11B


```
CTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAG
L  P  N  L  G  C  P  N  P  R  L  V  K  V  T  G  Q  C  C  E

GAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTT
E  W  V  C  D  E  D  S  I  K  D  P  M  E  D  Q  D  G  L  L

GGCAAGGGGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATT
G  K  G  L  G  F  D  A  S  E  V  E  L  T  R  N  N  E  L  I

GCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATC
A  V  G  K  G  S  S  L  K  R  L  P  V  F  G  M  E  P  R  I

CTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGC
L  Y  N  P  L  Q  G  Q  K  C  I  V  Q  T  T  S  W  S  Q  C

TCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGC
S  K  T  C  G  T  G  I  S  T  R  V  T  N  D  N  P  E  C  R

CTTGTGAAAGAAACCCGGATTTGTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGC
L  V  K  E  T  R  I  C  E  V  R  P  C  G  Q  P  V  Y  S  S
```

Figure 11C
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```
CTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACT
L  K  K  G  K  K  C  S  K  T  K  K  S  P  E  P  V  R  F  T

TACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGAC
Y  A  G  C  L  S  V  K  K  Y  R  P  K  Y  C  G  S  C  V  D

GGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCCCTGCGAAGAT
G  R  C  C  T  P  Q  L  T  R  T  V  K  M  R  F  P  C  E  D

GGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTCCAAATGCAACTACAACTGC
G  E  T  F  S  K  N  V  M  M  I  Q  S  S  K  C  N  Y  N  C

CCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCCAATGA
P  H  A  N  E  A  A  F  P  F  Y  R  L  F  Q  .
```